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Neutrokinin- α

1 AAATTCAGGATAACTCTCCTGAGGGGTGAGCCAAGCCCTGCCATGTAGTGCACGCAGGAC 60

61 ATCAACAAACACAGATAACAGGAAATGATCCATTCCCTGTGGTCACTTATTCTAAAGGCC 120

121 CCAACCTTCAAAGTTCAAGTAGTGATATGGATGACTCCACAGAAAGGGAGCAGTCACGCC 180
1 M D D S T E R E Q S R L 12

181 TTACTTCTTGCCTTAAGAAAAGAGAAGAAAATGAAACTGAAGGAGTGTGTTCCATCCTCC 240
13 T S C L K K R E E M K L K E C V S I L P 32
CD-I

241 CACGGAAGGAAAGCCCCCTCTGTCCGATCCTCCAAAGACGGAAAGCTGCTGGCTGCAACCT 300
33 R K E S P S Y R S S K D G K L L A A T L 52
CD-I

301 TGCTGCTGGCACTGCTGTCTTGCTGCCTCACGGTGGTGTCTTCTACCAGGTGGCCGCC 360
53 L L A L L S C C L T V V S F Y Q V A A L 72

361 TGCAAGGGGACCTGGCCAGCCTCCGGGCAGAGCTGCAGGGCCACCACGCCAGAAGCTGC 420
73 O G D L A S L R A E L Q G H H A E K L P 92
CD-II

421 CAGCAGGGAGCAGGAGCCCCAAGGCCGGCCTGGAGGAAGCTCCAGCTGTCACCGCCGGAC 480
93 A G A G A P K A G L E E A P A V T A G L 112
CD-III

#

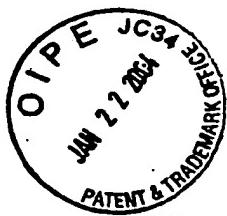
481 TGAAAATCTTGAACCACCAAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAGAAATA 540
113 K I F E P P A P G E G N S S Q N S R N K 132

541 AGCGTGCCGTTCAAGGGTCCAGAAGAAACAGTCACTCAAGACTGCTTGCAACTGATTGCAG 600
133 R A V Q G P E E T V T Q D C L Q L I A D 152
CD-IV

FIG. 1A

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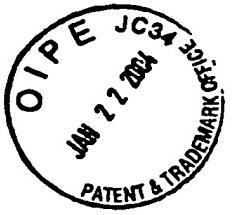
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Neutrokin- α

601	ACAGTGAAACACCAACTATACAAAAGGATCTTACACATTGTTCCATGGCTTCAGCT	660
153	<u>S E T P T I Q K G S Y T F V P W L L S F</u>	172
		CD-V
661	TTAAAAGGGGAAGTGCCCTAGAAGAAAAAGAGAATAAAATATTGGTCAAAGAAACTGGTT	720
173	<u>K R G S A L E E K E N K I L V K E T G Y</u>	192
		CD-VI
721	ACTTTTTATATGGTCAGGTTTATATACTGATAAGACCTACGCCATGGGACATCTAA	780
193	<u>F F I Y G O V L Y T D K T Y A M G H L I</u>	212
		CD-VII
781	TTCAGAGGAAGAAGGTCCATGTCCTGGGATGAATTGAGTCTGGTACCTTGTTCGAT	840
213	<u>Q R K K V H V F G D E L S L V T L F R C</u>	232
		CD-VIII
841	GTATTCAAAATATGCCTGAAAACACTACCCAATAATT CCTGCTATTCAAGCTGGCATTGCAA	900
233	<u>I O N M P E T L P N N S C Y S A G I A K</u>	252
		CD-IX
901	AACTGGAAAGAAGGAGATGAACCTCAACTTGCAATACCAAGAGAAAATGCACAAATATCAC	960
253	<u>L E E G D E L O L A I P R E N A Q I S L</u>	272
		CD-X
961	TGGATGGAGATGTCACATTTGGTGCAATTGAAACTGCTGTGACCTACTTACACCATGT	1020
273	<u>D G D V T F F G A L K L L</u>	285
		CD-XI
1021	CTGTAGCTATTTCTCCCTTCTGTACCTCTAAGAAGAAAATCTAACTGAAAATA	1080
1081	CCAAAAAAA 1100	

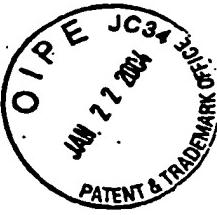
FIG. 1B

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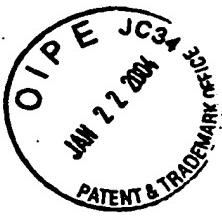
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FIG. 2A



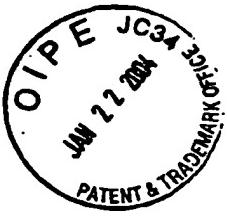
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FIG. 2B



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EIG. 2C



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	280	290	300	
193	P I Y L G G V F Q L E K G D R L S A E I N R P D Y L D F A E	TNFalpha		
166	S M Y H G A A F Q L T Q G D Q L S T H T D G I P H L V L S P	TNFbeta		
204	S V G F G G G L V Q L R R G E R V Y V N I S H P D M V D F A R	LTBeta		
242	S S Y T L G A V F N L T S A D H E T V N V S E L S L V N F E E	FasLigand		
244	S C Y S A G I A K L E E G D E L Q L A I P R E N A Q I S L D	Neutrokinne alpha		
225	S C Y S A G I A K L E E G D E L Q L A I P R E N A Q I S L D	Neutrokinne alphaS		
223	S G Q V Y F G I I A L	TNFalpha		
196	S - T V F F G A F A L	TNFbeta		
234	- G K T F F G A V M V G	LTBeta		
272	S - Q T F F G L Y K L	FasLigand		
274	G D V T F F G A L K L	Neutrokinne alpha		
255	G D V T F F G A L K L	Neutrokinne alphaS		

FIG. 2D

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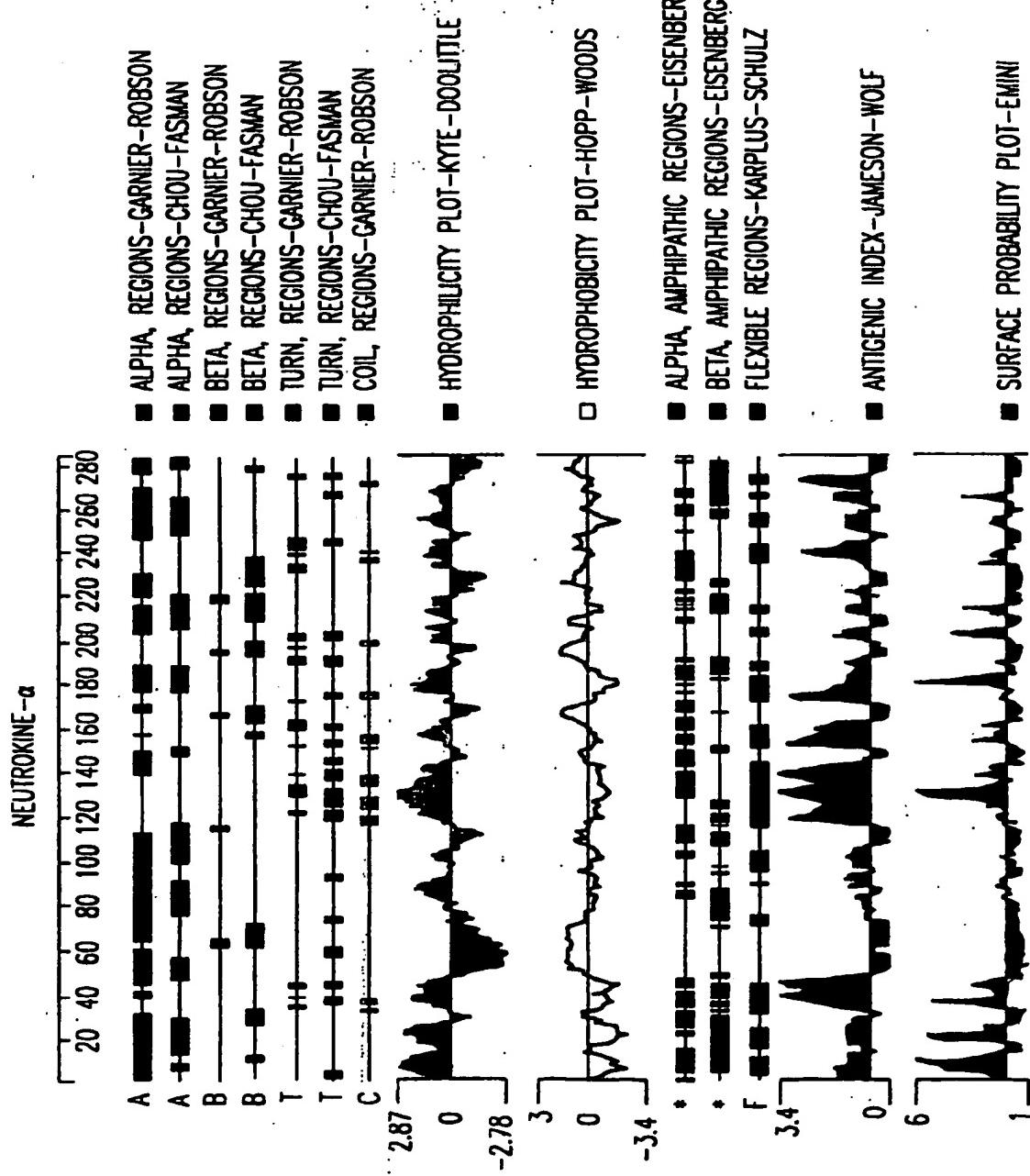


FIG. 3

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	1	50
HSOAD55RA GGNTAACTCT CCTGAGGGGT GAGCCAAGCC CTGCCATGTA	
HNEDU15X	...AAATTCA GGATAACTCT CCTGAGGGGT GAGCCAAGCC CTGCCATGTA	
HSLAH84R	.AATTGGCA NAGNAAACTG GTTACTTTT TATATATGGT CAGGTTTAT	
HLTBM08R	AATTCGGCAC GAGCAAGGCC GGCTGGAGG AAGCTCCAGC TGTCACCGCG	
	51	100
HSOAD55R	GTGCACGCAG GACATCANCA A..ACACANN NNNCAGGAAA TAATCCATT	
HNEDU15X	GTGCACGCAG GACATCAACA A..ACACAGA TAACAGGAAA TGATCCATT	
HSLAH84R	ATACTGATAA GACCTACGCC ATGGGACATC TAGTTAGAG GAAGAAGGTC	
HLTBM08R	GGACTGAAAA TCTTGAAACC ACCAGCTCCA GGAGAAGGCA ACTCCAGTCA	
	101	150
HSOAD55R	CCTGTGGTCA CTTATTCTAA AGGCCCAAC CTTCAAAGTT CAAGTAGTGA	
HNEDU15X	CCTGTGGTCA CTTATTCTAA AGGCCCAAC CTTCAAAGTT CAAGTAGTGA	
HSLAH84R	CATGTCTTG GGGATGAATT GAGTCTGGTG ACTTTGTTTC GATGTATTCA	
HLTBM08R	GAACAGCAGA AATAAGCGTG CCGTTAGGG TCCAGAAGAA ACAGTCACTC	
	151	200
HSOAD55R	TATGGATGAC TCCACAGAAA GGGAGCAGTC ACGCCTTACT TCTTGCCTTA	
HNEDU15X	TATGGATGAC TCCACAGAAA GGGAGCAGTC ACGCCTTACT TCTTGCCTTA	
HSLAH84R	AAATATGCC GAAACACTAC CCAATAATTCTGCTATTCA GCTGGCATTG	
HLTBM08R	AAGACTGCTT GCAACTGNNT GCAAGACAGTG AAACACCAAC TATACAAAAA	
	201	250
HSOAD55R	AGAAAAGAGA AGAAATGAAA CTGNAAGGAG TGTGTTCCA TCCTCCCACG	
HNEDU15X	AGAAAAGAGA AGAAATGAAA CT.GAAGGAG TGTGTTCCA TCCTCCCACG	
HSLAH84R	CAAACCTGGN AGGAAGGA... GATGAAC TCCAACTTGC AATACCAGGG	
HLTBM08R	GGCTCCCTTC TGNTGCCACA TTTGGGCCAA GGAATGGAGA GATTCTTCG	
	251	300
HSOAD55R	GAAGGAAAGC CCCTCTNTCC GATCCTCCAA AGACGGAAAG CTGCTGGCTG	
HNEDU15X	GAAGGAAAGC CCCTCTGTCC GATCCTCCAA AGACGGAAAG CTGCTGGCTG	
HSLAH84R	GAAAATGCAC AATTATCACT GGGATGGAGA TGTTCACATT TTTGGGTGC	
HLTBM08R	TCTGGAAACA TTTGCCAAA CTCTTCAGAT ACTCTTNCT CTCTGGGAAT	
	301	350
HSOAD55R	CAACCTTGNT GNTGGCATTG TGTTCTTGCT GNCTCAAGGT GGTGTTNTT.	
HNEDU15X	CAACCTTGCT GCTGGCACTG CTGTCTTGCT GCCTCACGGT GGTGTCCTTC	
HSLAH84R	CATTGAAACT GCTGTGACCT NCTTACANCA NGTGCTGTTN GCTATTTNC	
HLTBM08R	CAAAGGAAAA TCTCTACTTA GATTNACACA TTTGTTCCA TGGGTNTCTT	
	351	400
HSOAD55R	
HNEDU15X	TACCAAGGTGG CCGCCCTGCA AGGGGACCTG GCCAGCCTCC GGGCAGAGCT	
HSLAH84R	CTNCCTNTTC TNTGGTAACC TCTTAGGAAG GAAGGATTCT TAACTGGGAA	
HLTBM08R	AAGTTTAAA AGGGGAGTGC CCTTAGGAGG AAAAGGGAT AAATATTGGC	

FIG.4A

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	401	450
HSOAD55R HNEDU15X HSLAH84R HLTBM08R	GCAGGGCCAC CACGCGGAGA AGCTGCCAGC AGGAGCAGGA GCCCCCCAAGG ATAACCCAAA AAAANNTTAA ANGGGTANGN GNNAANGNG GGGNNNGTTNN CAAGGNACTG GTTANTTTNT AAATATGGTC AGGTTNTAT ANCTGGTAGG	
	451	500
HSOAD55R HNEDU15X HSLAH84R HLTBM08R	CCGGCCTGGA GGAAGCTCCA GCTGTACCG CGGGACTGAA AATCTTTGAA CNNGNNNNNT TTTNGGNNTA TNTNTNNNTN GGGNNNNNTA AAAATGGGGC CCTCGCCATG GGCATTNATT CANGNGAGG NCNNTCTTTT GGGNTGA...	
	501	550
HSOAD55R HNEDU15X HSLAH84R HLTBM08R	CCACCAAGCTC GAGGAGAAGG CAACTCCAGT CAGAACAGCA GAAATAAGCG CNANGGGGN TTTTT	
	551	600
HSOAD55R HNEDU15X HSLAH84R HLTBM08R	TGCCGTTCAAG GGTCCAGAAG AACAGTCAC TCAAGACTGC TTGCAACTGA	
	601	650
HSOAD55R HNEDU15X HSLAH84R HLTBM08R	TTGCAGACAG TGAAACACCA ACTATACAAA AAGGATCTTA CACATTTGTT	
	651	700
HSOAD55R HNEDU15X HSLAH84R HLTBM08R	CCATGGCTTC TCAGCTTAA AAGGGGAAGT GCCCTAGAAG AAAAAGAGAA	
	701	750
HSOAD55R HNEDU15X HSLAH84R HLTBM08R	TAAAATATTG GTCAAAGAAA CTGGTTACTT TTTTATATAT GGTCAAGGTTT	
	751	800
HSOAD55R HNEDU15X HSLAH84R HLTBM08R	TATATACTGA TAAGACCTAC GCCATGGGAC ATCTAATTCA GAGGAAGAAG	

FIG.4B

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801		850
HSOAD55R	
HNEDU15X	GTCCATGTCT TTGGGGATGA ATTGAGTCTG GTGACTTGT TTCGATGTAT	
HSLAH84R	
HLTBM08R	
851		900
HSOAD55R	
HNEDU15X	TCAAAATATG CCTGAAACAC TACCCAATAA TTCCCTGCTAT TCAGCTGGCA	
HSLAH84R	
HLTBM08R	
901		950
HSOAD55R	
HNEDU15X	TTGCAAAACT GGAAGAAGGA GATGAACTCC AACTTGCAAT ACCAAGAGAA	
HSLAH84R	
HLTBM08R	
951		1000
HSOAD55R	
HNEDU15X	AATGCACAAA TATCACTGGA TGGAGATGTC ACATTTTTG GTGCATTGAA	
HSLAH84R	
HLTBM08R	
1001		1050
HSOAD55R	
HNEDU15X	ACTGCTGTGA CCTACTTACA CCATGTCTGT AGCTATTTTC CTCCCTTTCT	
HSLAH84R	
HLTBM08R	
1051		1100
HSOAD55R	
HNEDU15X	CTGTACCTCT AAGAAGAAAG AATCTAACTG AAAATACCAA AAAAAAAAAA	
HSLAH84R	
HLTBM08R	
1101		
HSOAD55R	
HNEDU15X	AAAAAA	
HSLAH84R	
HLTBM08R	

FIG.4C

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Neutrokin- α SV

1 ATGGATGACTCCACAGAAAGGGAGCAGTCACGCCCTACTTCTGCCTTAAGAAAAGAGAA 60
 1 M D D S T E R E Q S R L T S C L K K R E 20

61 GAAATGAAACTGAAGGAGTGTGTTCCATCCTCCCACGGAAGGAAAGCCCCTGTCCGA 120
 21 E M K L K E C V S I L P R K E S P S V R 40
 CD-I

121 TCCTCCAAAGACGGAAAGCTGCTGGCTGCAACCTTGCTGGCACTGCTGTCTGCTGC 180
 41 S S K D G K L L A A T L L I A L L S C C 60
 CD-I

181 CTCACGGTGGTGTCTTCTACCAGGTGGCCGCCCTGCAAGGGGACCTGGCCAGCCTCCGG 240
 61 L T V V S F Y Q V A A L Q G D L A S L R 80
 CD-II

241 GCAGAGCTGCAGGGCCACCA CGCGGAGAAGCTGCCAGCAGGAGCAGGAGCCCCAAGGCC 300
 81 A E L Q G H H A E K L P A G A G A P K A 100
 CD-II CD-III

301 GG CCTGGAGGAAGCTCCAGTCAGCACCGCGGGACTGAAAATCTTGAAACCACCAAGCTCCA 360
 101 G L E E A P A V T A G L K I F E P P A P 120
 CD-III

 361 GGAGAAGGCAACTCCAGTCAGAACAGCAGAAATAAGCGTGCCGTTAGGGTCCAGAAGAA 420
 121 G E G N S S Q N S R N K R A V Q G P E E 140

421 ACAGGATCTTACACATTGTTCCATGGCTTCTCAGCTTAAAAGGGAGTGCCTAGAA 480
 141 T G S Y T F V P W L L S F K R G S A L E 160
 CD-IV

481 GAAAAAGAGAATAAAATATTGGTCAAAGAAACTGGTTACTTTTTATATATGGTCAGGTT 540
 161 E K E N K I L V K E T G Y F F I Y G O V 180
 CD-IV CD-V

541 TTATATACTGATAAGACCTACGCCATGGACATCTAATTAGAGGAAGAAGGTCCATGTC 600
 181 L Y T D K T Y A M G H L I Q R K K V H V 200
 CD-VI CD-VII

FIG.5A

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Neutrokin- α SV

601	TTTGGGGATGAATTGAGTCTGGTACTTTGTTCGATGTATTCAAAATATGCCTGAAACA	660
201	<u>F G D E L S L V T L F R C I O N M P E T</u>	220
	CD-VIII	CD-VIII
661	CTACCCAATAATTCTGCTATTCACTGGCATTGCAAAACTGGAAGAAGGAGATGAACTC	720
221	<u>L P N N S C Y S A G I A K L E E G D E L</u>	240
	CD-IX	CD-X
721	CAACTTGCAATACCAAGAGAAAATGCACAAATATCACTGGATGGAGATGTCACATTTTT	780
241	<u>Q L A I P R E N A Q I S L D G D V T F F</u>	260
	CD-X	CD-XI
781	GGTGCATTGAAACTGCTGTGACCTACTTACACCATGTCAGCTATTTCCCTCCCTTC	840
261	<u>G A L K L L</u>	266
	CD-XI	
841	TCTGTACCTCTAAGAAGAAAATCTAACTGAAAATACCAAAAAAAAAAAAAAAA	900
901	AAA 903	

FIG.5B

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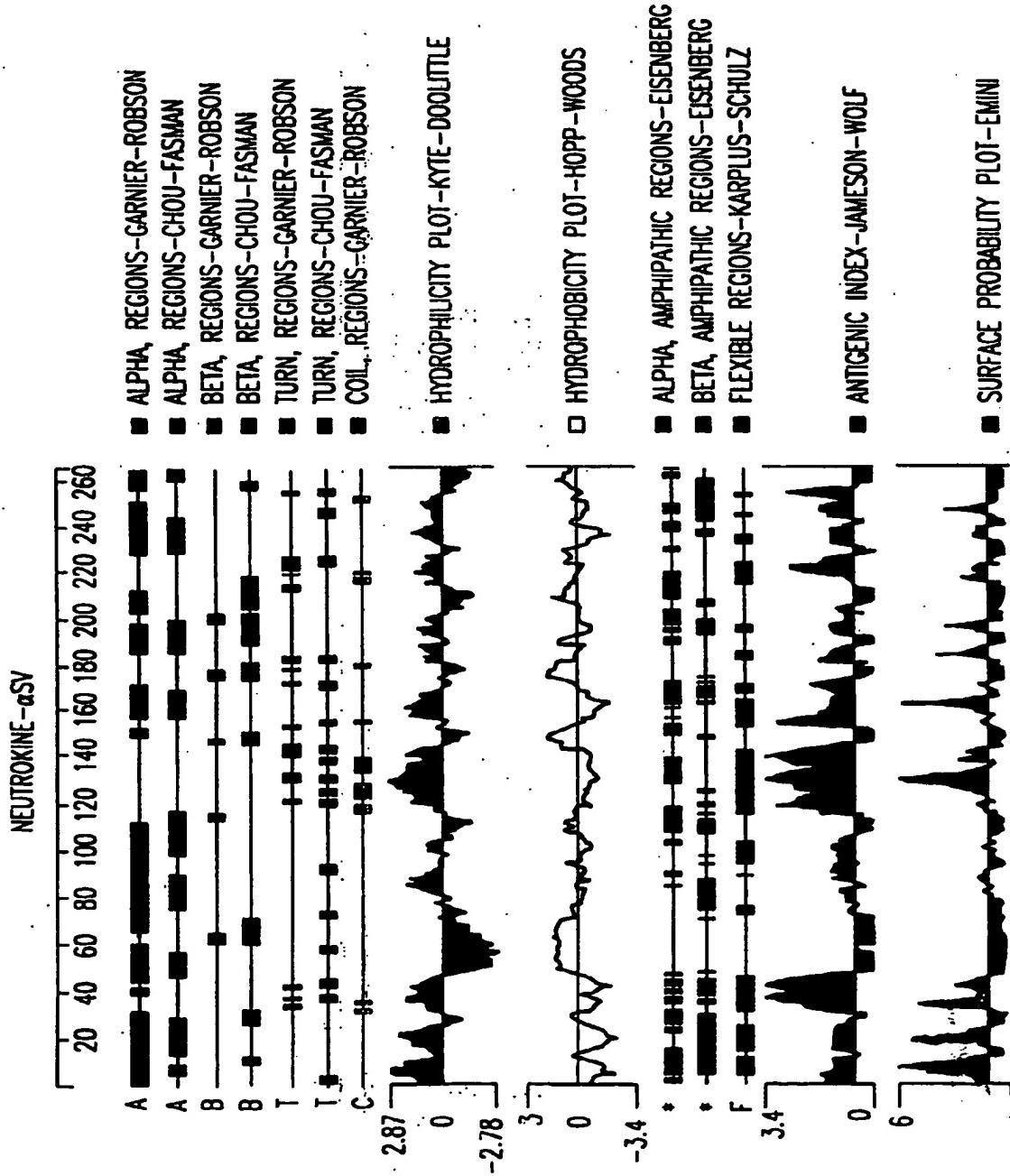


FIG. 6

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